



PCT09

## RAW SEQUENCE LISTING

DATE: 06/04/2002

PATENT APPLICATION: US/09/701,586B

TIME: 15:53:49

Input Set : A:\701586sq

Output Set: N:\CRF3\06042002\I701586B.raw

Pf.  
**ENTERED**

3 <110> APPLICANT: Kock, Michael  
 4 Hoeger, Thomas  
 5 Kroeger, Burkhard  
 6 Otterbach, Bernd  
 7 Lubisch, Wilfried  
 8 Lemaire, Hans-Georg  
 10 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene  
 12 <130> FILE REFERENCE: 0050/49100  
 14 <140> CURRENT APPLICATION NUMBER: US 09/701,586B  
 15 <141> CURRENT FILING DATE: 2002-04-25  
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889  
 18 <151> PRIOR FILING DATE: 1999-06-04  
 20 <160> NUMBER OF SEQ ID NOS: 33  
 22 <170> SOFTWARE: PatentIn/WordPerfect  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1843  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (3)...(1715)  
 32 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from brain tissue  
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 37 Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg  
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 40 gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa 95  
 41 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu  
 42 20 25 30  
 44 gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tgc 143  
 45 Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser  
 46 35 40 45  
 48 aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191  
 49 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu  
 50 50 55 60  
 52 gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239  
 53 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala  
 54 65 70 75  
 56 cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat 287  
 57 Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr  
 58 80 85 90 95  
 60 tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc 335  
 61 Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu

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62		100		105		110	
64	cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat						383
65	Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp						
66		115		120		125	
68	gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa						431
69	Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys						
70		130		135		140	
72	atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc						479
73	Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala						
74		145		150		155	
76	aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg						527
77	Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp						
78	160		165		170		175
80	gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta						575
81	Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu						
82		180		185		190	
84	cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa						623
85	Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys						
86		195		200		205	
88	gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt						671
89	Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu						
90		210		215		220	
92	cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa						719
93	Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu						
94		225		230		235	
96	gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg						767
97	Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly						
98	240		245		250		255
100	aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag						815
101	Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys						
102		260		265		270	
104	att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa						863
105	Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu						
106		275		280		285	
108	gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt						911
109	Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg						
110		290		295		300	
112	act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa						959
113	Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln						
114		305		310		315	
116	tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa						1007
117	Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys						
118	320		325		330		335
120	aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac						1055
121	Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn						
122		340		345		350	
124	cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa						1103
125	Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys						
126		355		360		365	

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128	gtg	att	tcc	cag	tac	cta	caa	tct	acc	cat	gct	ccc	aca	cac	agc	gac	1151
129	Val	Ile	Ser	Gln	Tyr	Leu	Gln	Ser	Thr	His	Ala	Pro	Thr	His	Ser	Asp	
130			370					375				380					
132	tat	acc	atg	acc	ttg	ctg	gat	ttg	ttt	gaa	gtg	gag	aag	gat	ggg	gag	1199
133	Tyr	Thr	Met	Thr	Leu	Leu	Asp	Leu	Phe	Glu	Val	Glu	Lys	Asp	Gly	Glu	
134		385					390					395					
136	aaa	gaa	gcc	ttc	aga	gag	gac	ctt	cat	aac	agg	atg	ctt	cta	tgg	cat	1247
137	Lys	Glu	Ala	Phe	Arg	Glu	Asp	Leu	His	Asn	Arg	Met	Leu	Leu	Trp	His	
138	400					405				410						415	
140	ggg	tcc	agg	atg	agt	aac	tgg	gtg	gga	atc	ttg	agc	cat	ggg	ctt	cga	1295
141	Gly	Ser	Arg	Met	Ser	Asn	Trp	Val	Gly	Ile	Leu	Ser	His	Gly	Leu	Arg	
142				420					425						430		
144	att	gcc	cca	cct	gaa	gct	ccc	atc	aca	ggg	tac	atg	ttt	ggg	aaa	gga	1343
145	Ile	Ala	Pro	Pro	Glu	Ala	Pro	Ile	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly	
146			435					440					445				
148	atc	tac	ttt	gct	gac	atg	tct	tcc	aag	agt	gcc	aat	tac	tgc	ttt	gcc	1391
149	Ile	Tyr	Phe	Ala	Asp	Met	Ser	Ser	Lys	Ser	Ala	Asn	Tyr	Cys	Phe	Ala	
150			450				455				460						
152	tct	cgc	cta	aag	aat	aca	gga	ctg	ctg	ctc	tta	tca	gag	gta	gct	cta	1439
153	Ser	Arg	Leu	Lys	Asn	Thr	Gly	Leu	Leu	Leu	Leu	Ser	Glu	Val	Ala	Leu	
154		465				470				475							
156	ggg	cag	tgt	aat	gaa	cta	cta	gag	gcc	aat	cct	aag	gcc	gaa	gga	ttg	1487
157	Gly	Gln	Cys	Asn	Glu	Leu	Leu	Glu	Ala	Asn	Pro	Lys	Ala	Glu	Gly	Leu	
158	480				485				490					495			
160	ctt	caa	ggg	aaa	cat	agc	acc	aag	ggg	ctg	ggc	aag	atg	gct	ccc	agt	1535
161	Leu	Gln	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Met	Ala	Pro	Ser	
162				500					505					510			
164	tct	gcc	cac	ttc	gtc	acc	ctg	aat	ggg	agt	aca	gtg	cca	tta	gga	cca	1583
165	Ser	Ala	His	Phe	Val	Thr	Leu	Asn	Gly	Ser	Thr	Val	Pro	Leu	Gly	Pro	
166			515						520					525			
168	gca	agt	gac	aca	gga	att	ctg	aat	cca	gat	ggg	tat	acc	ctc	aac	tac	1631
169	Ala	Ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr	
170			530					535					540				
172	aat	gaa	tat	att	gta	tat	aac	ccc	aac	cag	gtc	cgt	atg	cgg	tac	ctt	1679
173	Asn	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu	
174		545					550					555					
176	tta	aag	gtt	cag	ttt	aat	ttc	ctt	cag	ctg	tgg	tga	atgttgatat				1725
177	Leu	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp						
178	560				565				570								
180	taaataaaacc	agagatctga	tcttcaagca	agaaaataag	cagtgttgta	cttgtgaatt											1785
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196			20				25			30						
198	Ser	Ser	Pro	Ala	Lys	Lys	Thr	Arg	Arg	Cys	Gln	Arg	Gln	Glu	Ser	Lys
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204	Lys	Gln	Asp	Glu	Ser	Val	Lys	Ala	Leu	Leu	Leu	Lys	Gly	Lys	Ala	Pro
205	65					70					75					80
207	Val	Asp	Pro	Glu	Cys	Thr	Ala	Lys	Val	Gly	Lys	Ala	His	Val	Tyr	Cys
208					85					90					95	
210	Glu	Gly	Asn	Asp	Val	Tyr	Asp	Val	Met	Leu	Asn	Gln	Thr	Asn	Leu	Gln
211			100						105					110		
213	Phe	Asn	Asn	Asn	Lys	Tyr	Tyr	Leu	Ile	Gln	Leu	Leu	Glu	Asp	Asp	Ala
214			115					120					125			
216	Gln	Arg	Asn	Phe	Ser	Val	Trp	Met	Arg	Trp	Gly	Arg	Val	Gly	Lys	Met
217		130					135					140				
219	Gly	Gln	His	Ser	Leu	Val	Ala	Cys	Ser	Gly	Asn	Leu	Asn	Lys	Ala	Lys
220	145					150					155					160
222	Glu	Ile	Phe	Gln	Lys	Lys	Phe	Leu	Asp	Lys	Thr	Lys	Asn	Asn	Trp	Glu
223					165					170					175	
225	Asp	Arg	Glu	Lys	Phe	Glu	Lys	Val	Pro	Gly	Lys	Tyr	Asp	Met	Leu	Gln
226				180					185					190		
228	Met	Asp	Tyr	Ala	Thr	Asn	Thr	Gln	Asp	Glu	Glu	Glu	Thr	Lys	Lys	Glu
229			195					200					205			
231	Glu	Ser	Leu	Lys	Ser	Pro	Leu	Lys	Pro	Glu	Ser	Gln	Leu	Asp	Leu	Arg
232		210					215					220				
234	Val	Gln	Glu	Leu	Ile	Lys	Leu	Ile	Cys	Asn	Val	Gln	Ala	Met	Glu	Glu
235	225					230					235					240
237	Met	Met	Met	Glu	Met	Lys	Tyr	Asn	Thr	Lys	Lys	Ala	Pro	Leu	Gly	Lys
238					245					250					255	
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241				260					265					270		

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243	Glu	Asp	Cys	Ile	Arg	Ala	Gly	Gln	His	Gly	Arg	Ala	Leu	Met	Glu	Ala
244			275					280					285			
246	Cys	Asn	Glu	Phe	Tyr	Thr	Arg	Ile	Pro	His	Asp	Phe	Gly	Leu	Arg	Thr
247		290					295					300				
249	Pro	Pro	Leu	Ile	Arg	Thr	Gln	Lys	Glu	Leu	Ser	Glu	Lys	Ile	Gln	Leu
250	305					310					315					320
252	Leu	Glu	Ala	Leu	Gly	Asp	Ile	Glu	Ile	Ala	Ile	Lys	Leu	Val	Lys	Thr
253				325						330					335	
255	Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg	Asn	Leu
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258	His	Cys	Ala	Leu	Arg	Pro	Leu	Asp	His	Glu	Ser	Tyr	Glu	Phe	Lys	Val
259			355					360					365			
261	Ile	Ser	Gln	Tyr	Leu	Gln	Ser	Thr	His	Ala	Pro	Thr	His	Ser	Asp	Tyr
262		370					375					380				
264	Thr	Met	Thr	Leu	Leu	Asp	Leu	Phe	Glu	Val	Glu	Lys	Asp	Gly	Glu	Lys
265	385					390					395					400
267	Glu	Ala	Phe	Arg	Glu	Asp	Leu	His	Asn	Arg	Met	Leu	Leu	Trp	His	Gly
268					405					410					415	

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270 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
271          420          425          430
273 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
274          435          440          445
276 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
277          450          455          460
279 Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly
280 465          470          475          480
282 Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
283          485          490          495
285 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
286          500          505          510
288 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
289          515          520          525
291 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
292          530          535          540
294 Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
295 545          550          555          560
297 Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
298          565          570

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301 &lt;210&gt; SEQ ID NO: 3

302 &lt;211&gt; LENGTH: 2265

303 &lt;212&gt; TYPE: DNA

304 &lt;213&gt; ORGANISM: Homo sapiens

306 &lt;220&gt; FEATURE:

307 &lt;221&gt; NAME/KEY: CDS

308 &lt;222&gt; LOCATION: (242)...(1843)

309 &lt;223&gt; OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from uterus tissue

311 &lt;400&gt; SEQUENCE: 3

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315 tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattg ttgggaattc      120
317 tctccctaata tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag      180
319 gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc tttctctggc      240
321 c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag      286
322 Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu
323 1          5          10          15
325 aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc tcc      334
326 Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser
327          20          25          30
329 acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc cgc      382
330 Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg
331          35          40          45
333 gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg tat      430
334 Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr
335          50          55          60
337 gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac aac      478
338 Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn
339          65          70          75
341 aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc      526

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RAW SEQUENCE LISTING ERROR SUMMARY  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:17; Xaa Pos. 26,27,33,34,35,38,39,40,41,42,43  
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Seq#:19; Xaa Pos. 2,3,4,6,7,9,13,15,16  
Seq#:20; Xaa Pos. 2,3,4,6  
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